

In the **Specification**, please enter the following amendments.

On page 18, before the first full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1           5           10          15
Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
          20          25          30
Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
          35          40          45
Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
          50          55          60
Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65          70          75          80
Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
          85          90          95
Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
          100         105         110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
          115         120         125
Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
          130         135         140
Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145          150          155          160

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Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
195 200 205
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
210 215 220
Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
245 250 255
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
290 295 300
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
305 310 315 320
Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335
Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
 370 375 380
 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
 385 390 395 400
 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
 405 410 415
 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
 420 425 430
 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
 435 440 445
 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
 450 455 460
 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
 465 470 475 480
 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
 485 490 495
 Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser
 500 505 510
 Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu
 515 520 525
 Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu
 530 535 540
 His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
 545 550 555 560
 Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu
 565 570 575
 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

580 585 590
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu
595 600 605
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
610 615 620
Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
625 630 635 640
Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
645 650 655
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
660 665 670
Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala
675 680 685
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
690 695 700
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
705 710 715 720
Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
725 730 735
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
740 745 750
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
755 760 765
Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)
770 775

--Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

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atgatccttg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag      60
aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg      120
ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc      180
agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg      240
gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata      300
aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac      360
ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc      420
gacatcgaga cgctctacca cgagggagaa gagtttgga cggggccgat tctgatgata      480
agctacgccg atgaaagcga ggcgcgctg ataacctgga agaagatcga ccttccttac      540
gttgagggtt tctccaccga gaaggagatg attaagcgct tcttgagggt cgtaaggag      600
aaggaccgga acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa      660
aagcgctgtg agaagcttgg cgtgagcttt accctcggga gggacgggag cgagccgaag      720
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gcgggttttc gcaagcccaa ggagaaggtc tacgccgagg agatagccac cgcctgggag      900
accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac      960
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gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaaa cgtctcgcca     1260
gatacgctca accgcgaggg gtgtaggagc tacgacgttg ccccgagggt cggtcacaag     1320
ttctgcaagg acttccccgg cttcattccg agcctgctcg gaaacctgct ggaggaaagg     1380
cagaagataa agaggaagat gaaggcaact ctcgaccgcg tggagaagaa tctcctcgat     1440
tacaggcaac gcgccatcaa gattctcgcc aacagctact acggctacta cggctatgcc     1500
agggcaagat ggtactgcag ggagtgcgcc gagagcgtaa cggcatgggg aagggagtac     1560
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atcgaaatgg tcatcagaga gcttgaggaa aagttcgggtt ttaaagtcct ctatgcagac 1620
acagacggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca 1680
atggagttct taaactatat caatcccaa ctgcccggcc ttctcgaact cgaatacgag 1740
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ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag 1860
gagacgcagg cgagggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgctc 1920
agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg 1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc 2100
tacatcgttc tgaagggctc cggaaggata ggcgacaggg cgattccctt cgacgagttc 2160
gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca 2220
gttgagagaa tcctcagggc cttcggctac cgcaaggaag acctgcgcta ccagaagacg 2280
aggcaggtcg ggcttggcgc gtggctgaag ccgaagggga agaagaagtg a 2331 (SEQ ID NO: 11)
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